

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 5, 2002, 14:57:02 ; Search time 534.27 Seconds  
(without alignments)  
12732.167 Million cell updates/sec

17352.167 Million cell updates/sec

Title: US-08-153-397a-1  
Perfect score: 3962  
Sequence: 1 CGGGCCGGAAGTGGGGTGA.....AAAAAAGGGAATTC 3962

Scoring table: IDENTITY\_NUC 1  
Gapop 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N.Geneseq\_032802:\*

- 1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
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- 19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
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- 21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001.DAT:\*
- 23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3962	100.0	3962	18	AAAT93785
2	3960.4	100.0	3962	16	AAQ92520
3	3960.4	100.0	3962	16	AAQ92522
4	3617.6	91.3	3754	16	AAQ84782
5	3383.2	85.4	3554	24	AA516842
6	2783.6	70.3	2861	21	AAQ99051
7	2783.6	70.3	2861	22	AAH33198
8	642	16.2	3096	19	AAV48292
9	642	16.2	3157	16	AAQ92521

10	642	16.2	3157	16	AAQ92523	Human colonic aden
11	642	16.2	3157	18	AAAT93784	CCR-2, a human mam
12	639.8	16.1	3120	19	AAV55895	Receptor protein t
13	639.8	16.1	3120	20	AAV55895	Receptor protein t
14	544.2	13.7	2725	22	AAH99505	Human protein enco
15	522.8	13.2	563	23	AA557829	CDNA #505 encoding
16	453.4	11.4	2128	15	AAQ64158	Partial coding seq
17	324.4	8.2	408	21	AAQ00624	Human secreted pro
18	236	6.0	272	16	AAAT2477	Human gene signatu
19	228.4	5.8	463	22	ABA43008	Human breast cell
20	228.4	5.8	463	22	ABA53422	Human foetal liver
21	228.4	5.8	463	22	ABA23197	Human brain expres
22	228.4	5.8	463	22	AAK01693	Human bone marrow
23	228.4	5.8	463	22	AAK27141	Human bone marrow
24	228.4	5.8	463	22	AAI11731	Probe #1664 for ge
25	228.4	5.8	463	22	AAI33038	Probe #1724 used t
26	228.4	5.8	463	22	AAI01659	Probe #1650 used t
27	182.2	4.6	2820	16	AAAT5156	gd.trkB fusion use
28	180.6	4.6	1746	23	AA584464	DNA encoding novel
29	180.6	4.6	2301	19	AAV20445	Human c-trk oncoge
30	180.6	4.6	2301	21	AAQ03303	Human trk oncogene
31	180.6	4.6	3060	16	AAAT51457	Human trk oncogene
32	180.6	4.6	3194	21	AAZ88839	Human trkB recepto
33	180.6	4.6	3707	17	AAQ99277	Human trkB recepto
34	180.6	4.6	2526	15	AAQ69029	Human neurotrophic
35	180.2	4.5	2526	13	AAQ28668	Porcine TrkC gene.
36	178.6	4.5	2526	14	AAQ34581	Encodes adult porc
37	178.6	4.5	2526	16	AAAT51458	trkC clone in pRL
38	178.6	4.5	2940	16	AAAT51458	gd.trkB fusion use
39	177	4.5	2750	20	AAK87599	DNA coding for neu
40	158	4.0	4092	20	AAV70230	Human receptor tyr
41	151	3.8	175	22	ABA48136	Human breast cell
42	151	3.8	175	22	ABA66013	Human foetal liver
43	151	3.8	175	22	ABA33099	Probe #11565 for g
44	151	3.8	175	22	AAK14437	Human brain expres
45	151	3.8	175	22	AAK40171	Human bone marrow

## ALIGNMENTS

RESULT 1  
AAAT93785 standard; CDNA; 3962 BP.

AAAT93785;  
16-FEB-1998 (first entry)

Human mammary carcinoma kinase 10 (MCK-10) cDNA sequence.  
Mammary carcinoma kinase; MCK-10; receptor tyrosine kinase;  
Proliferative disease; cancer; Insulin receptor family;  
tyrosine kinase neurotrophin receptor; MCK-10 activity;  
neurological disorder; aberrant expression; ds.

Homo sapiens.

Key CDS Location/Qualifiers  
321..307 /\*tag= a

US5677144-A.

14-OCT-1997.

08-NOV-1994; 94US-0336343.

16-NOV-1993; 93US-0153397.

(ALVE/) ALVES F H E.

(ULTR/) ULLRICH A.



[illegible][illegible]

QY 3901 GCCTAGCAGGTATTAATAAGCTTTCACCAAAAAAAAAACCGGAT 3960  
 DB 3901 gcactagcaggtataataaagcttgcttcacacaaaaaaaaaacggat 3960  
 QY 3961 TC 3962  
 DB 3961 tc 3962

RESULT 2  
 ID AA092520 standard; cDNA to mRNA; 3962 BP.  
 AA092520;  
 26-NOV-1995 (first entry) 1  
 Human mammary carcinoma kinase 10 (MCK-10) cDNA.  
 Mammary carcinoma kinase 10; transmembrane receptor;  
 receptor tyrosine kinase; cancer; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 321..3080  
 FT /\*tag- a  
 FT misc\_difference 2315  
 FT /\*tag- b  
 FT /\*note- "some clones have 6 AA deletion here"  
 XX MO9514088-A.  
 XX 26-MAY-1995.  
 XX 16-NOV-1994; 94MO-EP03797.  
 XX 16-NOV-1993; 93US-0153397.  
 XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX Alves FHE, Ullrich A;  
 XX WPI; 1995-224054/29.  
 XX P-PSDB; AAR75502.  
 XX New nucleic acid encoding MCK-10 receptor tyrosine kinase - and  
 XX derived vectors, transformed cells, proteins and antibodies useful  
 XX for diagnosis and treatment of proliferative disease, esp. cancer,  
 XX and for screening modulators  
 XX Claim 4; Page 50-52; 115pp; English.  
 XX cDNA prep'd. from human breast cancer cell line MCF7 (ATCC HTB22) and  
 XX used in a PCR with two degenerate oligo primer pools based on  
 XX conserved sequences of the kinase domain of receptor tyrosine  
 XX kinases. One clone, designated MCK-10, was identified as novel RTK.  
 XX The PCR fragment was used to screen a lambda gtl1 library of human  
 XX fetal brain cDNA. Several overlapping clones were identified. The  
 XX composite of these cDNA clones is given in AA092520 and the deduced AA  
 XX sequence in AAR75502. Some of the clones had a deletion of 6 AAs at  
 XX posn. 2315 in the MCK-10 sequence. MCK-10 has all the  
 XX characteristics of a receptor PK (see AAR75502 FT). Screening of  
 XX human placental library yielded two cDNA clones MCK-10-1 and  
 XX MCK-10-2. One of the clones isolated from the human fetal brain  
 XX library cont'd. an additional 18 nts in the TK domain. The MCK-10 splice  
 XX isoforms have been designated MCK-10-1 (with an additional 111 bp  
 XX between nts 1832 and 1943); MCK-10-2 (without any insertions); MCK-10-3  
 XX (with the additional 111 bp and and 18 bp in the TK domain); and MCK10-4  
 XX (with the additional 18 bp). The predicted mol. wts. of MCK-10-1 and  
 XX MCK-10-2 preceptors are 101.13 and 97.17 kd respectively, and can thus  
 XX be subdivided into a 34.31 kd alpha subunit and and 66.84 or 62.88 kd

CC beta subunits that contain the TK homology and alternative splice sites.  
 XX  
 SQ Sequence 3962 BP; 735 A; 1235 C; 1181 G; 811 T; 0 other;  
 Query Match 100.0%; Score 3960.4; DB 16; Length 3962;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3961; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCTGAGACTGGGCTGACTGGGACCTAGAGAAATCTGAGTGAGGCCCCGAGAG 60  
 DB 1 cgggcctgagactgggctgactgggacctaagagaaatctgagtgagggccccgagag 60  
 QY 61 CTGCTCTCGGAGAGCGCCCTCCGACACCCGAGCCCGCGCGCTCCCGCTCCGCGCTC 120  
 DB 61 ctgctctcggagagcgccctccgacacccgagcccgcgcgctcccgctcccgctc 120  
 QY 121 CCGGCTCCTGGCTCCCTCCGCTCCCGCTCCCGCTCCCGCTCCCGCTCCCGCT 180  
 DB 121 cggctcctggctccctccgctcccgctcccgctcccgctcccgctcccgctcc 180  
 QY 181 CCGGGTGGAGCGCTGGGCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
 DB 181 ccgggtggagcgctgggctggcgagagagagagagagagagagagagagagagag 240  
 QY 241 TCACTGACGATGGGGTTTGACTTGAAGAAATGCCAAGATGCTGCCACCCCTTA 300  
 DB 241 tcactgacgatggggttgacttgaagaaatgccaaagatgctgccaccacctta 300  
 QY 301 GGGCCGAGGATCAGAGAGCTATGGAGACAGGCCCTGTCACTTACTGCTGCTCT 360  
 DB 301 gggccgaggatcagagagctatggagacagggccctgtcacttactgctgctct 360  
 QY 361 TGGTGGCAAGTGGAGATCTGATGATGAGGAGACATTTGATCTGAGGCGGCTGTG 420  
 DB 361 tggtggaagtggagatctgatgatgagagacatTTGATCTGAGGCGGCTGTG 420  
 QY 421 CCCTGGGATCAGAGACCGAGCAATCCAGACAGTACATCTGCTTCCAGCTCTGTG 480  
 DB 421 ccctgggatcagagaccgagcaatccagacagTACATCTGCTTCCAGCTCTGTG 480  
 QY 481 CAGATTCACCTGCCGCCGCCGACAGAGAGTTGGAGAGATGAGAGGAGATGGGCTGTG 540  
 DB 481 cagatTCACCTGCCGCCGCCGACAGAGAGTTGGAGAGATGAGAGGAGATGGGCTGTG 540  
 QY 541 GCGCCGAGGGGTGGTGTTCGCAAGAGAGAGAGTACTTCAGGTGATGTACACGAC 600  
 DB 541 gcccgcaggggtgggtgttcgcaagagagagTACTTCAGGTGATGTACACGAC 600  
 QY 601 TCACCTGTGTGCTCTGTGTGGGACCCAGGAGCGGATCCGGGGGCTTGGCAAGAGT 660  
 DB 601 tcacctgtgtgctctgtgtgggacccagagcgGATCCGGGGGCTTGGCAAGAGT 660  
 QY 661 TCTCCCGAGCTACCGGCTGGCTGATCTCCCGAGTGTGCGCGCTGATGGGCTGGAAG 720  
 DB 661 tctcccgagctaccggctggctgatctcccgagtGTGCGCGCTGATGGGCTGGAAG 720  
 QY 721 ACCCGTGGGGCAGAGAGATGATCTCAGGCAATGAGACCCGAGAGAGATGGTGTGAAG 780  
 DB 721 acccgTGGGGCAGAGAGATGATCTCAGGCAATGAGACCCGAGAGAGATGGTGTGAAG 780  
 QY 781 ACCTTGAGCCCCCATGATGATCCGAGCTGTTCCTTACCCCGGGGCTGACCGGCTCA 840  
 DB 781 accttgagcccccatgattgattccgagctgtTCCTTACCCCGGGGCTGACCGGCTCA 840  
 QY 841 TGAATGTCTGCTCTCGGGGTAGAGCTCTATAGGCTCCTCTGAGAGAGATGATCTCTGTT 900  
 DB 841 tgaatgtctgctctcggggtagagctctatagGCTCCTCTGAGAGAGATGATCTCTGTT 900  
 QY 901 ACACCGCCCTGTGTGGGCGACAGCAATGATTATATGAGCGCGTACTTACAGACATCA 960  
 DB 901 acacgcctctgtgtggcgacagcaatgatttatTATGAGCGCGTACTTACAGACATCA 960

QY	961	CCTATGAGGAGATACCGTGGGCGGAGCTGCACTATGAGGGGCTGTGGGCCAGCTGGCAGATG	1020
Db	961	cctatgagagacatccgtgsgagactgcaatgaggggtcttggccagctgsgagatg	1020
QY	1021	GTTGATGAGGGCTGGAATCACTTTAGGAAGATGACAGACTGGGGTCTGGCCAGGCTATG	1080
Db	1021	gttgatgagggctggaatactttaggaagatgacagactgggggtctggccaggctatg	1080
QY	1081	ACTATGAGGATGAGAGCAACCAAGACTTCTCAGTGGGCTATGATGAGATGGATTGAGT	1140
Db	1081	actatgaggatgagagcaaccagacttctcagtggtgatagtgagatgagattgaggt	1140
QY	1141	TTGACCGGCTAGAGGCGCTTCCAGGCTATGAGGTCACTGTAAACAATGACACAGCTGAG	1200
Db	1141	ttagccgcttagagggccttcacaggctatgacaggtccactgttaacaactgcaacagctg	1200
QY	1201	GAGCCGCTGCTGGGGGGGTGAATGCTTCCTTCGGCGTGGGCGCTTCGATGGCTTGGG	1260
Db	1201	gagccgcttgcgcgcggcggtggaatgcttccttcggcggtggcgcttcgactgtgcagctg	1260
QY	1261	AGGGGAGAGCCCATGCGCACAACCTAGGGGGCAACCTGGGGAGACCCAGACCGCGGCTG	1320
Db	1261	aggggagagcccatgcgcaacaacctaggggcaacctggggagacccagagccgggctg	1320
QY	1321	TTTCAGTGGCCCTTGGGGGCGGTGTGGCTTCTTCTGACATGGCCGCTTCTCTTTGGG	1380
Db	1321	tctcagtgcccccttggggcggtgtggcttcttcttgacatggccgcttctctcttggg	1380
QY	1381	GGGCTGATTACTTTCAGGGAATTCCTTCATCTCGATGATGATGATGAAATTCCTTC	1440
Db	1381	ggcctgttatcttctcaggaatacttccttcatactctgatagtgtgaacaattccttc	1440
QY	1441	CGGCACTGGGAGGACACTTCCCGCAGCCCGCTGGTGGCGGCTGGGCCACACTCCACA	1500
Db	1441	cggcactgggaggaacactccgcagcccgctgtggcgcgccgtggccacctccaca	1500
QY	1501	AGTTACACACTTGGAGACTGAGAGGCCAGAGGCCAGACCCGCTGGCCAGGCGGAGA	1560
Db	1501	acttcacacacttggagactgagagggccagagccagccggtggccaagggcgaaggga	1560
QY	1561	GGCCGAGCCGATCTTCATGAGGTGCTGTGGGCAATCATCTGCTGCTGTGCTATCA	1620
Db	1561	ggccgagccgcatctcatatgctgtgctgtgtgacataccctgctctcgtctcatca	1620
QY	1621	TTGCGCTCATGCTCTGGCGGCTGCATGCGGCGAGAGCTCTCAGCAGAGCTGAACGAGGG	1680
Db	1621	ttagccctcatgctctggcggtgcatacgcgagcgtccctcaggaagctgaaaggggg	1680
QY	1681	TGTTGGAAGAGGAGTGAAGCTTCACTCTCTGCTCCCTGGGAGACATCTCTCATACA	1740
Db	1681	tgttggaaagagggctgaagcttcaactctctgcccgtgggacatactctcaaca	1740
QY	1741	ACCGCAGAGTCTTAGAGAGCACCCCGTACAGAGAGCCCGGCGCTGTGGGAATCGCG	1800
Db	1741	accgccagtgctcttagagagcaccccgtaacagagagcccgcgctgtggaatccgc	1800
QY	1801	CCGACTTCGCTCTCTGTGTCGCCAATGAGCTCTGCGTTGCTCTCCAAATCCAGCCTAAC	1860
Db	1801	ccgacttcgctctctgtgtcccaatgagcttgcgttgcctccaaatccagcctaacc	1860
QY	1861	GGCTCTTGTGGGCAATTAGCGCCGTCGCCCTGAGAGCCCGGGCGCCGCCACACCGGCT	1920
Db	1861	ggctcttgtgggcaattagcgccgtgccctgagagcccgggccccccacacacggcct	1920
QY	1921	GGGCGCAAAACCAACACACCAAGGCTTAGAGTGGGACTATATGAGAGCTGAGAAGCAG	1980
Db	1921	gggcgcaaaaccaaacacacacaggtctagagtgggactatatagggcctgagaaacag	1980
QY	1981	GGGCGCGGCTTGTGCCCCCACTGCCAAGACGCTGCCCATTAATGCCGAGGCTGACA	2040
Db	1981	ggcgccggcttgtgcccccaactgccaaagacagctgcccatltagcgaagctgaca	2040
QY	2041	TGTATTACCTGCAGGGCGTACACGGGGGCAACACTATGCTGTGCTGTGCATGCCCCAG	2100
Db	2041	tgttaacctgcagggcgtaacgggggcaaacatactgtgtgcctgcactgccccag	2100
QY	2101	GGGCACTGGGGATGGCCCCCAGAGTGAATTTCTCTGATCTGATCTCCGCTTCAAG	2160
Db	2101	gggcactgggatggccccagagtgaatttctctgatctgatctccgcttcaag	2160
QY	2161	AGAACTTGGGAGGGCCAGTTTGGGGAGGTGACACTGTGTGAGTGCAGACCCCTCAAG	2220
Db	2161	agaaacttggagggccagtttggggaggtgacactgtgtgagtgtagagccctcaag	2220
QY	2221	ATCTGTCAGTCTGATTTCCCGCTTAATGTCGTAAGGACACCCCTTGTGCTGAGTG	2280
Db	2221	atctgtcagctctgatttcccccttaatgtcgtgaaggagacaccttgtctgttagctg	2280
QY	2281	TCAGATCTTACGGGCAAGTGCACCAAGAAATGCGAGCTTCTGCTGTTCTCCAGGAATG	2340
Db	2281	tcaगतctttagggcaagtgcaccaagaatagtccagttcttcttcttcccggaatg	2340
QY	2341	ATTTCCTAAAGAGGTGAAGATTCATGTGAGAGCTTCAGAGACCCCAATCATTCGGCTGC	2400
Db	2341	atttcctaaagaggtgaagattcatgtgagagcttcagagaccccaatcattcggctgc	2400
QY	2401	TGGCGTGTGTGTGACAGACACACCCCTCTGATGATTAATCACTGATACATGAGAACGGCG	2460
Db	2401	tggcggtgtgtgtgacagacacacccctctgatgattaatcactgatatgagaacggcg	2460
QY	2461	ACCTTCACACAGTTCCTCACTGATCCACACAGCTGAGAGACAGCGAGGGGCGCCCTG	2520
Db	2461	accttcacacagttcctcagtgcacacagctgagagacagcgagcgaggggccctg	2520
QY	2521	GGGAGCGGCAAGCTGCGGAGGGGCGACCAATCACTACCTACCTGCTGTGATGTGGCAG	2580
Db	2521	gggagcggcaagctgcggaggggcgaccaatcactacctgctgtgatgtggcag	2580
QY	2581	CCGAGATCGCCTCCGGCATGCGCTATGTGCGCACTCAACTTTGTATCGGAGACCTGG	2640
Db	2581	ccgagatcgccctccggcatgcgctatgtgcgcaactcaactttgtatcgcggagacctgg	2640
QY	2641	CCAGCGCGAAGTGCCTAGTTGGGAAAAATTTACCACTCAAAAATGCAAGACTTTGGCATGA	2700
Db	2641	ccaгcgcgaaagtgcctagttgggaaaaattccaactcaaaaatgcagactttgcatga	2700
QY	2701	GCCGGAACCTCTATGCTGGGGGCAATTACGTTGTGAGGGCGCGGCGAGTCTGCCATCC	2760
Db	2701	gccggaaaccttatgctgggggcaattacgttgtgagggcgcgagctgcgcatacc	2760
QY	2761	GCTGATGAGCTGGAGTGCATCCTCATGAGGGAATTCACAGACTGCGAGTGAAGTGGGG	2820
Db	2761	gctgatgagctggagtgcatcctcataggggaattcacagactgcgagtgaagtgggg	2820
QY	2821	CCTTTGCTGAGCCCTTGGGAGAGTGTGATGCTCTGTAGAGCCCAAGCCTTTTGGCAGC	2880
Db	2821	cctttgtgtagcccttgggagagtgtgattgctctgttagagcccaagccttttggcagc	2880
QY	2881	TCACCGACGAGAGGTGATGAGAACCGGGGGAG	

D	3121	gggaagcagtgacactaaacaagygacacatgcaacctctgccttccctccgga	3180
Q	3181	CAGGCCATCACTCTTAATAGAGCACTGAGACTGCAGTGGGCTGGGCCACACAGGGAG	3240
D	3181	cagcccaaccctcaataatagacatgagactgcaagygctgggcccaccccaaggag	3240
Q	3241	CTGATGCCCTTCTCCCTCCCTCCGAGACACTCATGTCCTCCCTTCCTGTTCTCTCC	3300
D	3241	ctgagtcaccttctccctctcccttcctggagcaaacctcatcttcccttccgttcttcc	3300
Q	3301	TAGAAGCCCTGTGTCGCCACCCAGCTGGTCTGTGGATGGATCCTCTCCACCCCTCT	3360
D	3301	tagaagagccctctgcgcacccacccagctggtccctgtgatgtagtctctccacccctct	3360
Q	3361	AGCCATCCCTGGGGGAAAGGTGGGGGAAATATAGATAGACATCGACATAGGCCCATG	3420
D	3361	agccatccctctgggaaaggttgggggaaatatagatatagacaactgagacagcccatg	3420
Q	3421	GAGCACTGGGGCCCACTGGACACACATGATTCTGTGAAGGTGGCTCGGCCAGCTTC	3480
D	3421	gagacactggggcccaactggaacaacatgattcttcggagaggttggctcgccccaagctc	3480
Q	3481	TCTCTCCCTGTCAACACTGAGACCCACCTGCTGAGAACTCTGGGGGTAGAGAGACAAG	3540
D	3481	tctctccctgtcaacaactggaaccccaactggtctggaatctgggttagagagacaaga	3540
Q	3541	AGGAGAGGAAAATGTTCTCTTGCTGTGCTCTCTCTGTACTTGTACTCAGTTGGGCTTC	3600
D	3541	aggagaggaataatgttctctctgtgctgtcctgtaactgttccctagcttggcttcc	3600
Q	3601	CTCTCCATCCTGAAAGACTGGACCTGGGGGTAGCCCGGCCACGCCCTCAGTCAQC	3660
D	3601	ctctccatcctgaaaaccttgagacctgggttagcccgccagccctcagtaacc	3660
Q	3661	CCACTTCCCACTGGAGCTGTGTGAGTGAACCTTCTTAAGCTTACGTTTCTGTGGAG	3720
D	3661	ccacttcccaactgacgtctctgtagctaaacttcccaagcctataagttctctgtgag	3720
Q	3721	TAAATATTTGGATTGGGGGAAAAGAGGAGACAGGCCCATAGCTTGGGGTTGGACATC	3780
D	3721	taaatatttgatttgggggaaaggggagcaagcccatagccttgggttgtagatc	3780
Q	3781	TCAAGTGAACCTGCCACATTTGATTTTTCTAATAATACATTGGGGTTGTACATTTTGGG	3840
D	3781	tcaagttagactgcacatatttcttcataataccttgggttctgtacatttltggg	3840
Q	3841	GGAGAGACAGATTTTACATTAATATAGACTAGCTGAGGACATTTAATCCCT	3900
D	3841	gggagagacagatttctacataataatagaccttagcttggggcaatttaaccct	3900
Q	3901	GCACTAGGCAAGTAAATTAATTAAGTTGAGTTTCCACAAAAAATAAAAAACGGAAAT	3960
D	3901	gcactagagcagtaataataaagtttagtttccacaaaaataaaaaaaccggaat	3960
Q	3961	TC 3962	
D	3961	tc 3962	

RESULT	3
AA092522	
ID	AA092522 standard; cDNA to mRNA; 3962 BP.
XX	
XX	
AC	AA092522;
XX	
DT	26-NOV-1995 (first entry)
XX	
DE	Human mammary carcinoma kinase 10 (MCK-10) cDNA.
KW	
KW	Mammary carcinoma kinase 10; MCK-10; transmembrane receptor,
KW	receptor tyrosine kinase; cancer; ss.
XX	
OS	Homo sapiens.

XX		
FH	Key	Location/Qualifiers
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FT		/tag= a
FT	misc_difference	2315
FTm		/tag= b
XX		/note= "some clones have AA deletion here"
PN	W09514089-A.	
PD		
XD	26-MAY-1995.	
XX		
PE	16-NOV-1994;	94MO-EP03799.
XX		
PR	16-NOV-1993:	93US-0153397.
XX		
PA	(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.	
XX		
PI	Alves FHE, Ullrich A;	
XX		
DR	WPI; 1995-224055/29.	
DR	P-PDB; AAR75504.	
XX		
PT	New nucleic acid encoding CCK-2 receptor tyrosine kinase - and derived vectors, transformed cells, proteins and antibodies, useful for diagnosis and treatment of proliferative and nervous system diseases and for screening modulators	
XX		
XS	Disclosure; Page 67-69; 115pp; English.	

CC cDNA p16d from human breast cancer cell line MCF7 (ATCC HTB22) was  
CC used in a PCR with two degenerate oligo primer pools based on  
CC conserved sequences of the kinase domain of receptor tyrosine  
CC kinases. One clone, designated MCK-10, was identified as novel RTK.  
CC The PCR fragment was used to screen a lambda gt11 library of human  
CC fetal brain cDNA. Several overlapping clones were identified. The  
CC composite of these cDNA clones is given in AA092822 and the deduced AA  
CC sequence in AAR75504. Some of the clones had a deletion of 6A at posn  
CC 2315 in MCK-10 sequence. MCK-10 has all the characteristics of  
CC a receptor PTK (see AAR75504 FT). Screening of human placental library  
CC yielded two cDNA clones. One of the clones isolated from the human  
CC fetal brain library contained an additional 18 nts in the TK  
CC domain. The MCK-10 splice isoforms were designated MCK-10-1  
CC (with an additional 111 bp between nts 1832 and 1943); MCK-10-2  
CC (without any insertions); MCK-10-3 (with the additional 111 bps and  
CC 18 bp in the TK domain); and MCK-10-4 (with the additional 18 bp).  
CC The predicted mol. wts. of MCK-10-1 and MCK-10-2 pre-receptors are  
CC 101.13 and 97.17 kD respectively, and can thus be subdivided into a  
CC 30.31 kD alpha subunit and a 66.84 or 62.86 kD beta subunits that  
CC contain the TK homology and alternative splice sites.

[illegible]

QY	241	TCAC	TGACGAGCGATGGGGTTGACATTGAAAGAAATGCCAAGAAATGCTGGCCCCACCCCTTA	300
Db	241	TCAC	TGACGAGCGATGGGGTTGACATTGAAAGAAATGCCAAGAAATGCTGGCCCCACCCCTTA	300
QY	301	GGCC	GGAGGGGATCAGAGACTATGGGACACAGGCCCTGTATCTTATCTGCTCTGCTCT	360
Db	301	GGCC	GGAGGGGATCAGAGACTATGGGACACAGGCCCTGTATCTTATCTGCTCTGCTCT	360
QY	361	TGGT	GGCAAGTGGAGATCTGACATGAAAGAGACATTTGATACCTGGCAGATGGCCGTAG	420
Db	361	TGGT	GGCAAGTGGAGATCTGACATGAAAGAGACATTTGATACCTGGCAGATGGCCGTAG	420
QY	421	CCCT	GGGATGCGAGACCGGACACATCCAGACATGACATCTGTGCTCCAGCTCTGCT	480
Db	421	CCCT	GGGATGCGAGACCGGACACATCCAGACATGACATCTGTGCTCCAGCTCTGCT	480
QY	481	CAGATT	CCACTGCGCCGCCACAGAGCTTGGAGAGACACTGACGGGAGATGGGCTGCT	540
Db	481	CAGATT	CCACTGCGCCGCCACAGAGCTTGGAGAGACACTGACGGGAGATGGGCTGCT	540
QY	541	GCCCG	GCAAGGGGCGGGTGTTCCTCCAAAGAGAGAGATCTTCGACGAGTGAATCAACAAG	600
Db	541	GCCCG	GCAAGGGGCGGGTGTTCCTCCAAAGAGAGAGATCTTCGACGAGTGAATCAACAAG	600
QY	601	TCCAC	CTGCTGCTGGTGGGACCCACAGGAGCGCATGCGGGGGGCTGGGGCAAGAAAT	660
Db	601	TCCAC	CTGCTGCTGGTGGGACCCACAGGAGCGCATGCGGGGGGCTGGGGCAAGAAAT	660
QY	661	TCTCC	CGGAGCTACCGGCTGCTACTCCCGGATGCTCGCGCTGATGGCTGGAGAG	720
Db	661	TCTCC	CGGAGCTACCGGCTGCTACTCCCGGATGCTCGCGCTGATGGCTGGAGAG	720
QY	721	ACCG	TGGGGTCAGAGAGGTGATCTCAGGCAATGAGACCTGAGGGAGTGGTCTGAGAG	780
Db	721	ACCG	TGGGGTCAGAGAGGTGATCTCAGGCAATGAGACCTGAGGGAGTGGTCTGAGAG	780
QY	781	ACCT	TGGGCCCCCATGATGTTGCCGATGAGTGGTTCCTACCCCGGCTGACCCGGTCA	840
Db	781	ACCT	TGGGCCCCCATGATGTTGCCGATGAGTGGTTCCTACCCCGGCTGACCCGGTCA	840
QY	841	TGAG	TGTGTCTCGCGGGTAGAGCTCTATGGCTGCTCTGGAGGATGGACTCTGTCTT	900
Db	841	TGAG	TGTGTGTCTCGCGGGTAGAGCTCTATGGCTGCTCTGGAGGATGGACTCTGTCTT	900
QY	901	ACAC	GGCCCCGTTGGGGGACAGATGATATTACTAGAGCCGTGACTCAACGACTCA	960
Db	901	ACAC	GGCCCCGTTGGGGGACAGATGATATTACTAGAGCCGTGACTCAACGACTCA	960
QY	961	CCTAT	GAGGACATACCGTGGGCGAGTGCAGATGATGGGGGCTGGGGCAGCTGGGAGATG	1020
Db	961	CCTAT	GAGGACATACCGTGGGCGAGTGCAGATGATGGGGGCTGGGGCAGCTGGGAGATG	1020
QY	1021	GTGT	GTGGGCTGTGATGACTTATAGAGAAAGTCCAGAGCTGCGGCTGTGGCCAGGCTATG	1080
Db	1021	GTGT	GTGGGCTGTGATGACTTATAGAGAAAGTCCAGAGCTGCGGCTGTGGCCAGGCTATG	1080
QY	1081	ACTAT	GTGGGATGGAGAAACACACAGCTCTCCACGATGGGCTATGTGAGATGGAGTTTGAGT	1140
Db	1081	ACTAT	GTGGGATGGAGAAACACACAGCTCTCCACGATGGGCTATGTGAGATGGAGTTTGAGT	1140
QY	1141	TTTG	ACCGGCTAGGGGCTTCACAGGCTATGCGAGTCCACGATGAACAATGACACAGCTGG	1200
Db	1141	TTTG	ACCGGCTAGGGGCTTCACAGGCTATGCGAGTCCACGATGAACAATGACACAGCTGG	1200
QY	1201	GAGC	CGCTGTGCTGTGGCGGGGTGAAATGTGCTTCGCGGGTGGCCCTGACATGAGCTTGG	1260
Db	1201	GAGC	CGCTGTGCTGTGGCGGGGTGAAATGTGCTTCGCGGGTGGCCCTGACATGAGCTTGG	1260
QY	1261	AGGG	GAGGCCCATGCGGCAACAACCTAGGGGGACACTGGGGGACCCCAAGACCGGGCTG	1320
Db	1261	AGGG	GAGGCCCATGCGGCAACAACCTAGGGGGACACTGGGGGACCCCAAGACCGGGCTG	1320

QY	1321	TCGCAATGCCCTTGTGGCGCCGTGTGGCTGGCTTTCGCAAGTCCGCTCTCTTTCGGC	1380
Db	1321	ttcgcagtgcaccttbgcgcgctgtgctgcgtcttcctgtcagctgcgccttccttgcg	1380
QY	1381	GGCCCGGTACTCTTCAGAGGAATTCCTCATCTCTGATGTGGTGAACATTTCTCTC	1440
Db	1381	ggcccggtactactcttcgcgaatactctctactctgtgtgtgaaacaattctcttc	1440
QY	1441	CGGCAATGGGAAGCACACTTCCCGGACACCCCTAGTGGACGCGCTGGCCCACTCCACCA	1500
Db	1441	cggcaatgggaagcaacttcccggaacccctagtggtggacgcgctggccccaactccaca	1500
QY	1501	ACTTCAGACGCTTGAGCTGAGGCCAGAGGCCAGCGCCGTGGCCAGAGCCAGAGGGA	1560
Db	1501	acttcagacgcttgaagcttgaagccagagagccagcgccgtggccagagccagggga	1560
QY	1561	GGCCGACGCGCATCTCATTCGGCTGCCGTGGTGGGCATCAATCCGTCTCTGTGCTCAACA	1620
Db	1561	ggccgacgcgcatctctacatcggcttgggtgggcataatccgtctctgtgctcaaca	1620
QY	1621	TTGCGCTCATGCTCTGCGGCGGCTGCACTGGGAGCGGACGCTCAAGAGGCTGAACGAGAG	1680
Db	1621	ttgcgctcatgctctgcgggcgctgcactgggagcggtcctcctcagaaggtcgaagagag	1680
QY	1681	TGTGGAAAGAGAGCTGACGCTTACCTCTCTGTCTCCCTGGGGACACTATCTCATCAACA	1740
Db	1681	tgtggaagagagctgacgcttacctctctgtctccctggggacactatctcatcaaca	1740
QY	1741	ACCGGCCAGAGTCTTAGAGAGGCCACCCCGTACCAAGAGGCCCGGCTCGTGGGAATCCGC	1800
Db	1741	accggccagagtcttagagagccacccgtaaccaagagcccgctcgttggaaatccgc	1800
QY	1801	CCCACTCCGCTCCCTGATGCCCAATGGCTCTGCTGTCGTCGTCACATTCAGACCTTACC	1860
Db	1801	cccactccgctcctctggtgcccaatggctctgctgtctcgtctcctcaatcagactaac	1860
QY	1861	GCCTCTTCTGTGGCACTTACGCCCGTCCCTCTGAGAGCCCGGAGCCGCCACACCGGCT	1920
Db	1861	gcctcttctgtggcaacttacgcccgctccctctgagagcccgagcccccacaacccgct	1920
QY	1921	GGGCCCAACCCACCAACACCAGGCTTACAGTGGGACATATATGAGCCTGAGAACCCAG	1980
Db	1921	ggggcccaaacccaaccaaacccaaggtctaacagtgtggaactatgtgagcctgagaagccag	1980
QY	1981	GGGCCCGCCTTCTGGCCGCACCTCCCGAGAAAGAGGCTCCCGCATTAATGCCAGAGCTGACA	2040
Db	1981	ggggcccgcttctgtgcccacactctcccagaacaaggtccccaattatgtcgaggtgtgaca	2040
QY	2041	TTGTATACCTCTCAGAGGGGCTCACCGGGGGCAACACTATCTGTGCTCTACATGCCCCAG	2100
Db	2041	ttgtataacctctcagaggggctcacccgggggcaaacctatctgtgctctgacatgtcccag	2100
QY	2101	GGGCAGTGGGGAGTGGGCCCCGAGAGTGGATTTCCCTGATCTGACTCCGCTTCAAG	2160
Db	2101	gggcagtggggagtgggccccagagtggtattccctgactgactcgcgtctcaag	2160
QY	2161	AGAACTTGGGAGAGGGGACGTTTGGGAGGTGCACTGTGTGATGGATGCAAGCCCTCAAG	2220
Db	2161	agaaacttgggagaggggacagtttgggaggtgcacctgtgtgagtgcagacgcctcaac	2220
QY	2221	ATCTGGTCACTTGAATTTCCCTTAATGTGGGTAAAGGGAACCCCTTGTGTGTAGCTG	2280
Db	2221	atctggtcacttgaatttcccttaattgtgggtaaagggaaccccttgtgtgtagctg	2280
QY	2281	TCAAGATCTTACGGCGAGATGCCACAGAAATGCCAGTTCTCTTGTCTCAGAGATG	2340
Db	2281	tcaagatctttagcgcgagatgccacaagaatgccaagttctctctgtctccagagatg	2340
QY	2341	ATTTCCTGAAGAGGTGAATATGATATGCAAGGCTCAAGACCCCAACTCATTTGGGTGC	2400
Db	2341	atttcctgaagaggtgaatatgatatgcaaggctcaagaccccaactcatattgggtgc	2400
QY	2401	TGGCGTGTGTGTGTCAGAGAGACCCCTCTGTGATATTACTGACTATCGAGAAACGGC	2460



Db 2401 tgggcygtygtctgacgagagacccctctgcatactactgactacatgagaaagcg 2460  
 QY 2461 ACCTCAACAGTTCCTCAGTGCCACAGCTGAGAGCAAGGACGAGGGGGCCCTCG 2520  
 Db 2461 acctcaacaggtctccctcagtgcccaacagctgaaagaaagacgagcgagggccctcg 2520  
 QY 2521 GGGACGGGAGGCTGCGCAGAGGGCCACATCAGTACCCAAATGCTGCTCATGTGCGAG 2580  
 Db 2521 gggaaagcgagcgctgcagagggggcccaacatcagctacccaatgctgcatgtygcag 2580  
 QY 2581 CCCAGATCCGCTCCGGGAGATGCGGTATCTGCGCCACTCAACTTTGTACATCGGAGACTCG 2640  
 Db 2581 cccaagatcgctccgagcagtgctatctgcacactcaactctgtacactcgagactcg 2640  
 QY 2641 CCACGGGAACTGCTAGTGTGGGAAATTTACATCAAAATCGAGACTTTGGCATCA 2700  
 Db 2641 ccacgggaaactgctcagtggtgggaaatctcaacatcaaatcgagactctgagcatga 2700  
 QY 2701 GCCGGAACCTCTATGCTGGGAGTATTTACCGTGTGAGGGCGGCGGAGTGTGCCATCC 2760  
 Db 2701 gccggaaacctctatgctgggagctattaccgtgtgcagggccgggagtgctgcccacatc 2760  
 QY 2761 GCGGATGCGCTGGGAGTGCATCCCTATGAGGAAAGTTACGACTGCGAGTGAAGTGGG 2820  
 Db 2761 gctggatggcgctgggagtgcatctcctcaatgggaaagttcacgactgagtgacgtggg 2820  
 QY 2821 CCTTTGGTGTGACCCGTGTGAGAGTGTGATGCTGTGTGAGGGCCGACCTTTGGGCGAC 2880  
 Db 2821 cctttggtgtgacccgtgtgagagtgctgtatgctgtatggcccgaccttgggcaagc 2880  
 QY 2881 TCACGAGCAGCAGTGCATCGAAGAACGCGGGGAGTTCTTCGGGACAGGGCGGCGAG 2940  
 Db 2881 tcacgagcagcagtgatcagaaagcgggagtgcttccggagcagggccggcgag 2940  
 QY 2941 TGTACCTGTCCGGGCGCTGCTGCTGCGGAGGCGCTATATAGCTGATGCTTCGCTGCT 3000  
 Db 2941 tgaacctgtccggcgccgctgctgctgcgcaaggccctaatgagctgactcgtgctgct 3000  
 QY 3001 GGAGCGGGAGTCTGAGCAGCAGCACCCTTTTCCAGCTGATGCTGCTGCGCAGAG 3060  
 Db 3001 ggagcgggagtgctgagcagcgacacaccttccagtgatgctgctcggcgagag 3060  
 QY 3061 ATGCACTCAACAGGTGTATATCACAATCCAGTGCCTTCCTTCAGGAGTGAATCCAG 3120  
 Db 3061 atgcactcaacaggtgtgtatcacacatccagctgcccctcccaaggagtgtaccag 3120  
 QY 3121 GGGAGGCCAGTACTAATAAGAGAGACAAATGGACACTCTGCTCCCTCCCTCCCGA 3180  
 Db 3121 gggaaagccagtgacactaaacaaagagacaaatggacactctgcccctccctcccgag 3180  
 QY 3181 CAGCCCATCACCCTTAATAGAGCAGTGAAGTGCAGTGGGCTGGGCCACCCAGGGAG 3240  
 Db 3181 cagcccatcactcctaatatagagcagtgagactgagctgagctgagcccaacccagggag 3240  
 QY 3241 CTGATGCCCCCTTCCTCCCTCTGAGACACTCTCATGCTCCCTTCCTGTTCTTCCTTC 3300  
 Db 3241 ctgatgcccccttccctccctctcctgacacatctcatgttcccttcccttcttccctcc 3300  
 QY 3301 TAGAAGCCCTGTGCGCCACCCAGTGTGCTGATGGATGGATCTCTTCACCTTCCTCT 3360  
 Db 3301 tagaagccctgtgcgcccacccagctgtccgtgagtgagcttctccacccctccct 3360  
 QY 3361 AGCCATCCCTTGGGAGAGGTTGGGAGAAATATAGATAGACACTGAGCATGGCCCATTTG 3420  
 Db 3361 agccatcccttgggagaggggtgggagaaatataagataagacactgagcatggcccatgtg 3420  
 QY 3421 GAGCACTGTGGGCGCCACTGTGACACACTGATCTCTGAGAGGTGCTCGGCCAGCTTC 3480  
 Db 3421 gagcactgtggcgcccaactgtgacacactgattctcgtgagaggtgctgccccagcttc 3480  
 QY 3481 TCTCTCCCTGTACACACTGTGAGCCCACTGGCTGAGATCTGGGGGTGAGAGGACAGA 3540  
 Db 3481 tctctccctgtacacactgtgagcccaactgagccctgagatctggtgggtgagagacaga 3540

Db 3481 tctctccctgtacacactgagcccaactgagccctgagatctggtgggtgagagacaga 3540  
 QY 3541 AGGAGAGGAAATNGTTTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600  
 Db 3541 aggagaggaanaatgttctcttgcctgctgctgctgctgctgctgctgctgctgct 3600  
 QY 3601 CTCTCTCATCACCTGGAACACTGAGACTGAGGGGTAGCCCGGCCGACCCCTCAGTACCC 3660  
 Db 3601 ctctctcatcaccttgaaacactgagactgaggggtagcccgcccgccctcagtaacc 3660  
 QY 3661 CCACCTTCCCACTTGACAGTCTTGTAGCTAGAACTTCTTAAGCCTATACGTTTCTGTGAG 3720  
 Db 3661 ccacttcccaacttgacagctctgtagctagaacttctcctaagcctatagcttctgtgag 3720  
 QY 3721 TAAATTTGGGATTTGGGGGAAAGAGGAGCAACGGGCCATAGCCTTGGGGTTGGACATC 3780  
 Db 3721 taaatatggatctgggggaaagagagagcaagcccatagccttgggtgtgagacatc 3780  
 QY 3781 TCTAGTGTAGCTGCCACATTTGATTTTCTATATATCACTTGGGGTTGTACATTTTGGG 3840  
 Db 3781 tctagtgtagctggccacatgatttctcataatcacttgggggtgtgacatttgggg 3840  
 QY 3841 GGAAGACACAGATTTTACACTAATATATATGACCTAGCTTGAAGCAATTTTATCCCT 3900  
 Db 3841 ggaagacacagattttaccataatataagaccagcttggagcaattttaatccct 3900  
 QY 3901 GCACATGAGCAGGTAATTAATAGTGTGACTTTTCCCAAAAAAATTAATACCGGAT 3960  
 Db 3901 gcacatgagcaggtatataaagtgagtttcccaaaaaaataaaacccggaat 3960  
 QY 3961 TC 3962  
 Db 3961 tc 3962

RESULT 4  
 AA084782  
 ID AA084782 standard; DNA; 3754 BP.  
 XX  
 AC AA084782;  
 XX  
 DT 17-AUG-1995 (first entry)  
 DE  
 XX Protein-tyrosine-kinase PTK22.  
 KW Protein-tyrosine-kinase; PK; discoidin domain receptor; cancer;  
 KW breast tumor; mamma carcinoma; diagnosis; prognosis; therapy; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 142..2886  
 FT /\*tag= a  
 XX  
 PN WO9502187-A.  
 XX  
 PD 19-JAN-1995.  
 XX  
 PE 08-JUL-1994; 94WO-GB01480.  
 XX  
 PR 09-JUL-1993; 93GB-0014271.  
 XX  
 PA (CANC-) CANCER RES INST.  
 PA (WELL) WELLCOME FOUND LTD.  
 PI Barker KT, Crompton MR, Gusterson BA, Martindale JE;  
 PI Mitchell PJ, Page MJ, Spence P;  
 DR WPI: 1995-066591/09.  
 DR P-PSDB: AAR71100.  
 XX  
 PT Method for screening substances, using protein tyrosine kinase -  
 PT for potential utility as therapeutic agents for cancer



XX Claim 1; Page 26-30; 51pp; English  
PS

CC CDNA derived from tumor metastatic tissue was amplified using primers  
CC primers (given in AAQ04783-84) based on sequences (AA871101,  
CC associated with protein-tyrosine-kinases (PTK). Novel PTK22 was  
CC identified in an isolated subclone. The 3' sequence of PTK22 was  
CC obtained by reverse transcription (using the primer of AA084786) and  
CC PCR amplification (primers AA084787-88) of RNA of human breast  
CC carcinoma cell line MDA MG 468. The partial DNA sequence of PTK22  
CC is given in AA084782.

50 Sequence 3754 BP; 713 A; 1145 C; 1121 G; 775 T; 0 other;

Query Match	91.38;	Score 3617.6;	DB 16;	Length 3754;
Best Local Similarity	98.78;	Pred. No. 0;		
Matches 3728; Conservative	0;	Mismatches 19;	Indels 29;	Gaps 7

QY	181	CCCCGGGTCGAGCGCTCGGGGCTTCGCCGGGAGACGATGAAAGGTCTGTGAAGTGGCTAT	240
Db	2	CCGGTCTCGAGCCGCTGGTCTCTCGCCGGGAAAGCGAATGAAAGGTCTGTGAAGTGGCTAT	61
QY	241	TCACTGAGCGATGGGGTGTGGACTCTTGAAGGAGATGGCCAAGAGATGCTGGCCCCACCCCTTA	300
Db	62	TCaactgagcgaatggggtcttggaacttgaaggaatgccaaagaaatgcgcgccaccacctta	121
QY	301	GGCCCCAGGAGATCAGAGACTATGGGACACAGAGGCCCTGTATCTTTTACTGCTGCTGCT	360
Db	122	ggcccgaggagatcagagactatggagaccagagcccggtacattcttaactgctgctct	181
QY	361	TGGTGGCAATGGGAGAGCTGACATGAAGGCAATTTTGTATCCTGCCAAGTGGCGGTAG	420
Db	182	tggtggcaaatgggagagctgacatgaaggcaattttgtatcctgccaaagtgcgtatg	241
QY	421	CCCTGGGCAATGACAGAGACCGGACCATCCCAACAGTGAATCTGCTTCAGTCTCTGCT	480
Db	242	ccttgaggcaatgacagagaccggacatcccaacagtgacatctgtcttcaggtcctcgt	301
QY	481	CAGATTGCATGGCGCCCGCCACAGCAGATTGGGAGAGCAATGACGGGAGTGGGCGCTGG	540
Db	302	cagattcgaatggcgcccgccacagcaaggtctgagagcagtgacgcygggagatggcctgct	361
QY	541	GCCCCGAGGGGTGGGTCTTCCCAAGAGAGAGGAGTACTTGCAGGTGATCTTACAACGAC	600
Db	362	gccccgagagggtgggtcttcccaagagagaggtacttgacgtyggatcttaacaagc	421
QY	601	TCCACCGGTGGGCTCGGTGGGACCCACAGGAGACCGATCCCGGGGCTCTGGCAGAGACT	660
Db	422	tccaactgtyggtctcctcggtaggaaccaagagaaaggaatgcgggtggtccctggcaagagt	481
QY	661	TCTCCGGAAGCTACCGGCTGCTTACTCCCGGATGTTGGCGTGGATGGGCTGGAAAG	720
Db	482	tctccggagactaaccggtcgtgcttaactccgcgaatgctgcgcgctggatgggtctggaaag	541
QY	721	ACCGCTGGGGGTACGAGAGTGATCTCAGGCAATGAGACCCCTGAGGAGTGTGTGAAG	780
Db	542	accgctgggggtacgagagtgatctcaggaatgagaccctgagggatgtygctcgaag	601
QY	781	ACCTTGGGCCCCCAATGAGTGGCCCGACCTGGTTCGCTTACCCCGGGCTGACCGGCTCA	840
Db	602	accttgggcccccaatgagtgcccgactggttcgtcttgtaaccccggtctgaaccggtca	661
QY	841	TGAGTCTGTGTGCGCGGAGAGCTCTATGGGTGGGCTCGAGGGAGATGACCTCTGTCT	900
Db	662	tgagtgctgtctcgtcgggtgaagaccttaatgctgcctctcgaggagatgtaaccctgctat	721
QY	901	ACACGGCCCCCTGTGGGGACAGCAATGTATTATCTGAGGCCCTGTACCTCAACGACTCA	960
Db	722	aaacgcgccccctgtggggcagacaatgtatttatctcgaggcgtgtactcaacgactcca	781
QY	961	CCTATGACGGAATACCGTGGGCGAGCTGCAATAGGGGGTCTGGGCGAGCTGGCAGATG	1020

QY	2098	CAGGGCAGGTGGGGAGTGGCCCCCCCAGAGTGGATTTCCTCGATCTCGACTCCGCTTCA	2157
Db	1922	cagggcaggtggggagtgvgggccccccagagtggaattccctctgactcgaaccgcgttca	1981
QY	2158	AGGAGAAGCTTGCGGAGGCGGCACTTTTGGGAGGTGCACCTGTGTAGAGGCGACACGCTTC	2217
Db	1982	agggagaagcttgggagbaggccaaatttggggaggtgaaacctggtgtaggtgcagaccctc	2041
QY	2218	AAGATCTGGTCAGTCTTGATTTCCTTAATGTGCGTAAGGAGACCCCTTGTCTGTAG	2277
Db	2042	aagatctggttaagcttgattcttcccttaattgtgtgaaggagacaaccttgcgtgtag	2101
QY	2278	CTGTCAAGATCTTTCGGGCGGAGTGGCCAGACCAAGAAATGCCAGCTTCCTCTCTCCAGGA	2337
Db	2102	ctgtcaagaattcttaagccgagcaatgpracaagaagt-----ccagga	2143
QY	2338	ATGATTTCCTGAAAGAGGTGAATATGATGTGAGGTCAGAGGCCCAACATCATTTCCGC	2397
Db	2144	atgatttcctgaaagaggtgaaagataatgtgcaggtgcgaagaccacaacatcatctgc	2203
QY	2398	TGCTGGGCGTGTGTGTGCAGGAGACCCCTCTGCATGATTACTGACTACATGAGAAAG	2457
Db	2204	tgctgggctgtgtgtgcagagacacccctctgcatactactgaatacvtgagaaag	2263
QY	2458	GCGACCTCAACAGTTCCTCTAGTGGCCACACAGCTGGAGGACAAAGGACGCGAGGGGGCC	2517
Db	2264	gcgcacctcaaacagttcttccatgtgcacacagctctggaagacaagacccgaggggtcc	2323
QY	2518	CTGGGAGCAGGGCAGGCTGCGCCAGGGGCCACACATCAGCTACCAATGGTGTGCAATGTGG	2577
Db	2324	ctgggagagggcaggtcgtgcgcaagggtccacaacatcaacatgtctgcgaatggtg	2383
QY	2578	CAGCCAGATGTGCTCCGGCATGCGCTATCTGTGGCCACACTCAACTTTGTACATGGGACC	2637
Db	2384	cagccagatgtgcttccggcatgctgtatctgtggccacaactctgtacatcgggacc	2443
QY	2638	TGGCCAGCGGGAATGTGCTGTGGGAAAAATTACATCAATAATCGAGACTTTGGCA	2697
Db	2444	tggccagcggaactgtctgattgtgggaaaaattcacatccacataatcgaaagcttgcga	2503
QY	2698	TGAGCCGGAACTCTATGCTGTGGGACTATTACCGTGTGAGGGCCGAGCGCATGTGCGCA	2757
Db	2504	tgaagcggaaactctatgtctggggaactatlaacgtgtgaaggccgggcaatgctgcaca	2563
QY	2758	TCCCGTGGATGTGCTGGGAATGCATCTCTATGGGGAAGTTCCACACTGCGAGTGAAGTGT	2817
Db	2564	tcccgtagatgtgcttgggaatgcatctctatggggaagttccacactgcgagtgaaagt	2623
QY	2818	GGGCGTTTGGGTGATACCCCTTGGGAGGTGCTGATGCTGTGGGCGCAGCCCTTTGGGC	2877
Db	2664	gggcgcttgggtgatacccttgggaggtgctgatagtctgtgggccccagacccttttgggc	2683
QY	2878	AGCTCACGAGCAGCAGGTGATCGAAGAACGCGGGGAGTTCTTCGGAGCCAGGGCCGCG	2937
Db	2684	agctcacagcagcaggtgatactgagaacgcggggaggtcttccggagaccaagggccgc	2743
QY	2938	AGGTGTACCTGTCCCGGCCCTCTGCTGCGCCGAGGGCTTAATAGCTGATGCTTGCGT	2997
Db	2744	aggtgtacctgtcccgcccgctgctgcgcgcaaggcctataatgagctgattgcttgcgt	2803
QY	2998	GCTGGACCGGGAGTGTGACACGACGACACACCTTTTCCAGGTGAGTGGTTCCTGGAG	3057
Db	2804	gctggagccgggagctctgagcaagcgaacacctttccagagtgatcgtgttctctgcag	2863
QY	3058	AGGATGCACTTCACACGCGTGTGATACACATTCACAGCTGCCCTCCCTCAGGAGTGATC	3117
Db	2864	aggatgcaacttcaacaacggtgtgaatacaacatccagctgcctccctcccaaggagcgttc	2933
QY	3118	CAGGGGAAGCGCAGTGAACATGAAGAAAGAGGACACAAATGGACACCTGTG-CCCTTCCTCC	3176
Db	2924	caggggaaagcagtgacataaacaagaggaacaatggaacctctgcctctccctc	2983

	Accession	Gene	Location/Qualifiers
OY	3177	CCACAGGCCATCACCTCCTAAATAAGAGGGCATGAGACTGCAGGTGGGCGGCCAACCCAG	3236
Db	2984	ccgaacagcccatacaccctcaatagaaggagtgagactgca----ggctggggccccaccag	3039
OY	3237	GGAGCTGATGCCCCCTTCTCCCTTCCTCGAGACACACTCATGTCCCTTCATTCTTC	3296
Db	3040	ggaagctgtagccctctctcccttcctgtaaacacatctcatgtgcccttccgtttctcc	3099
OY	3297	TTCCTAAGAAGCCCCTGTGCCCAACCAGCTGGGCTCTGTGAATGGATTCCTTCCACCTTC	3356
Db	3100	tccctcagaagccccgcgtcgccaccaagctggtcccgtagatgggacctcctcacccac	3159
OY	3357	CTCTAGGCCATCCCTTTGGGGAAGGCTGGGAGAAAATATAGATAGACACTGACATGGCCC	3416
Db	3160	ccttagccaatccctctggggaaggtyggggagaatatatagatagacacctgaaatggccc	3219
OY	3417	ATTGAGACACTGGGCCCCCACCCTGAGACACACTGATTCCTTGAGAGGTGGCTGCG--CCCA	3475
Db	3220	attgagacacccctgggccccaccctggaacaacactgatctccggaagtggtctggccccca	3279
OY	3476	GCTTCTCTCCCTGTGCACACACTGGACCCCACTGGCTGTAGATCTGGGGGTAGAGGA	3535
Db	3280	gcttctctctccctgcaacaacctggacccacctggctgagaatccgggggvtgaaggagga	3339
OY	3536	CAGAAGAGAGAAAAATGTTTCTGTGTGCTGCTGCTCTACTTGTCTCAGCTTGCGGT	3595
Db	3340	caagaagagagagaanaatgtttccttgtcgtccctgtactgtgctcagtgctggcgt	3399
OY	3596	TCTTCTCTCTCCATACCTCGAANAACACTGGACCTGGGGGTAGGCCCCCCCAGCCCTCAGT	3655
Db	3400	tcttctctctccatcaacctgaaacactlgaacctggggtagccggccccagccctcagtl	3459
OY	3656	CA-CCCCCACTTCCCACTTGCACTGAGTCTTGTAGTAGTAACCTTCTTAAGCCATACGTTGT	3714
Db	3460	caccccccacttcccaacctgacgtctgtgagttagaacttctctaagcctatacgttctc	3519
OY	3715	GTGGAGTAATATTGGGATTTGGGGGGAAGAGGAGCAACGGCCCTTAGCCTTGGGGTTG	3774
Db	3520	gtggagtaaatatctggtatctggggggaagaaggagcaacggccctcctgaggggtgtg	3579
OY	3775	GACATCTCTAGTGTAGCTCCACATTTGATTTTCTTAATCACTTGAGGGTTGTACATTT	3834
Db	3580	gacatctctagtgtagctgcgcacatgtatcttctcataatcaact-gggtgtgtaaatlt	3638
OY	3835	TTGGGGGGAGAGACACAGATTTTTACACTAATATATAGACCTTAGCTTGAGCAATTTTAA	3894
Db	3639	tfggggggagagagacacaggtcttttacactataatctgacccctagcttggggcaatttaa	3698
OY	3895	TCCCTGTGCACTGAGCAGGTAATATATPAAGGTGAGTTTCCACAAAAAAAAAAAAA	3950
Db	3699	tccctgtcactgagagagtaataataaagtttgaagtttccacaaaaaaaaaaaaa	3754
<b>RESULT 5</b>			
ID	AAS16842	standard; CDNA; 3554 BP.	
XX	AAS16842;		
XX	14-FEB-2002 (first entry)		
DE	Human epithelial discoidin domain receptor 1 (YSG5) trke cDNA.		
KX	YSG5; YSG5; schizophtenia; chronic animal model; LCGU; netrin receptor;		
KW	calcium-independent glucose utilisation; phosphodiesterase 1-alpha; UNC5H1;		
KM	calciun-dependent alpha-latrotoxin receptor; CIRK; trke; synapsin 1A;		
KM	epithelial discoidin domain receptor 1; synapsin 1B; neuroleptic; ss;		
OS	tumour necrosis factor alpha; TNF-alpha; human.		
XX	Homo sapiens.		
TH	Key	Location/Qualifiers	
TF	CD5	46..2676	

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FT      /tag- a
FT      /product- "Human trke polypeptide"
XX      WO200175440-A2.
XX      11-OCT-2001.
XX      02-APR-2001; 2001WO-GB01486.
XX      31-MAR-2000; 2000GB-0007880.
XX      26-MAY-2000; 2000GB-0012768.
XX      (WELF-) WELFIDE CORP.
XX      Cochran S, Paterson G, Ohashi Y, Morris B, Pratt J;
XX      WPI: 2002-010813/01.
XX      P-PSDB: MAU10542.
XX      Novel chronic animal model of schizophrenia, useful for identifying
XX      anti-psychotic drugs and genes that are associated with schizophrenia
XX      Claim 1; Fig 7a; 79pp; English.
XX      The invention relates to YSG polynucleotide fragments for use in
XX      diagnosing and/or developing treatments for schizophrenia using chronic
XX      animal models. The polynucleotides and their encoded polypeptides are
XX      used for identification of compounds which modulate the expression of YSG
XX      sequences, leading to the manufacture of schizophrenia medications. The
XX      sequences can also be used for testing candidate compounds for any effect
XX      on the polypeptides. Anti-schizophrenic effects of a compound can be
XX      determined by measuring local cerebral glucose utilisation (LCGU) or
XX      comparing its expression level with that of a control group. The
XX      sequences are useful in the identification of genes associated with
XX      schizophrenic states and in the development of an antibody. The sequences
XX      of the invention include phosphodiesterase 1-alpha, calcium-independent
XX      alpha-latrotoxin receptors (CIRL)-1.2a3, epithelial discoidin domain
XX      receptor 1 (trke), netrin receptor (UNC5H1), synapsins 1A and 1B and
XX      tumour necrosis factor (TNF) alpha. This sequence represents human
XX      epithelial discoidin domain receptor 1, trke (YSG5) DNA.
XX      Sequence 3554 BP; 682 A; 1064 C; 1065 G; 743 T; 0 other:
XX
Query Match      85.4%; Score 3383.2; DB 24; Length 3554;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 3545; Conservative 0; Mismatches 3; Indels 130; Gaps 3;

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QY      637 ATCCGGGGGCTTGCCAAAGAGACTCTCCCGAGCTACCGGCTGCTTACTCCCGGAGT 696
DB      atgcgggggcttgccaaaggagttctccggggtacacggcgctgtctctccggagtg 421
QY      697 GTCGGCGCTGAGATGGGCTGGAAGACCGTGGGCTAGAGAGTATCTCAGCAATGAG 756
DB      gtccgctggatggtgctggaaggaccgctggtgtaagagtgatctcaggcaatgag 481
QY      757 ACCCTGAGGAGAGTGTGCTGAAGAGACTTGGGCGCCCGCATGGTGGCGAGCTGCTGCT 816
DB      accctgagagatggtgtcgaaggaccttggccccccatggtgcgcgagtgctgct 541
QY      817 TCTACCCCGGGCTGACCGGGTCTATGATGTCTGTCTGCGGGTAGAGCTATAGCTGCTG 876
DB      tctacccccggctgacccgggtctatgagtgtctgtctggttagagcctatgctgctc 601
QY      877 TCTGAGGAGATGAGTCCCTGCTTATACCGCCCTGTGGGCGAGACATGTATTATCTG 936
DB      tctgagaggatgagatccctgcttatacaccgccccttgggagacaatgtaattatctg 661
QY      937 AGGCGCTGACCTCAACGACTCCACCTATGAGGAGCATACCGGGCGGAGCTGAGTATG 996
DB      aggcgctgacctcaacgactccacctatgagagacatacgtggcgagacgcagatcg 721
QY      997 GGGGCTGGGCCAGCTGCGAGATGCTGTGGGCTGGATGACTTTAGGAAGATCAG 1056
DB      gggctggtggccagctgscagatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 781
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DB      actcgggctggcgagctatgactatgtggatgagagcaacacagcttctcagtg 841
QY      1117 GCTATGTGAGATGAGTGTGAGTTGACCGGCTAGAGGCTCTTCAGGCTATGAGTCTG 1176
DB      gctatgtgagatgagtggtgagttgacggctagagggcttccagggctatgagtgctc 901
QY      1177 ACTGTAAACAATGCAACACGCTGGAGACCCGCTGCTGCGGGGTGGAATGCTCCTTCC 1236
DB      actgttaacaataatgcaacacgctggagacccgctgctgcggggtggaatgctccttc 961
QY      1237 GGGCGGCGCTGCACTGGCGCTGGAGGGAGGCCATCGCCACAACCTAGGGGGCAAC 1296
DB      ggcgctgctgcaactggcgctggagggagggccatcgccacaacctagggggcaacc 1021
QY      1297 TGGGGAGCCCGCAGAGCCCGGGCTGCTCAGTACCCTTGGGGCGCGGTGGCTGCTTTC 1356
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QY      1357 TGCAGTCCCGCTCTCTTTGGCGGGCCCTGAGTTACTTTCAGGCAAAATCTCTTCATCT 1416
DB      tgcagtcccgctctctttggcgggccctgagttacttctcaggaatctcttcatct 1141
QY      1417 CTGATGTGATGAACAATTCCTCCGAGCACTGGAGAGCACTTCCCGCACCCCTTGCT 1476
DB      ctgatgtgatgaacaattcctccgagcactggagagcacttcccgcaccccttgct 1201
QY      1477 GGGCGCTGGGCCACTCTCCACCACTTCAGACAGCTTGGAGCTGAGGCCAGGCCAGC 1536
DB      ggcgctgggccactctccacacttcagacagcttggagctgagagccagagccagc 1261
QY      1537 AGCCCGTGGCCAAGGCGAGGAGAGCCGAGCCGCACTTCATGCGCTGCTGTGGCA 1596
DB      agcccggtggccaaggcgagagagccgagcccatctcatctcgtgctgtgtgcca 1321
QY      1597 TCATCTGCTCTCTGCTGCTATCTATGCTTCATGCTCTGCGGCTGCACTGGCGCAGGC 1656
DB      tcatctgctctctgctgctatctatgcttcattgcttcgctgctgctgctgctgctgct 1381
QY      1657 TCTCAGCAAGGCTGAGAGGAGGCTGTGGAAGAGAGCTGACGCTTACCTCTCTGCTGC 1716
DB      tcctcagcaaggctgagagagagctgtggaagagagctgagaggttcatctctctgtcc 1441
QY      1717 CTGGGGAACACTATCTCATCAACAACCGCCAGGTCTCTAGAGAGCAACCCCGTACAGG 1776

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Db 1442 ctgggacacatctccatcaacaacagccaggtccctagagagcccccagcag 1501  
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Db 1502 agcccgcgcgcgcyggaatccgcgccacccctccctcgtgtcccaatgagcct--- 1557  
QY 1837 TGCTGCTCTCCAAATCCAGCCTACCGCCTCTGCGCACTTAAGCCCGTCCCTCGAG 1896  
Db 1558 ----- 1557  
QY 1897 GCCCGGGCCCCCACCACCCCGCTGGCCAAACCACACCCAGCCTACAGTGGG 1956  
Db 1558 -----gctcaagtgagg 1570  
QY 1957 ACTATATGAGACCTGAGAAAGCCAGCCGCCCGCTTCTGCCCCCACTCCCAAGACGCG 2016  
Db 1571 actataatgagcctgaaagcagcgcccgctctctgcgccacccctcccaagacagcg 1630  
QY 2017 TCCCCCAATTATGCGGAGGCTGACATGTGTAACCTGACAGGGGCTCACCGGGGGCAACACT 2076  
Db 1631 tcccccatatgcccagagcctgacatgttaccctgcagggcggtcaaccggygacacact 1690  
QY 2077 ATGCTGTGCTGACACTGCCCCAGGGGCACTGGGGATGGGCCCCCAAGATGATTTCC 2136  
Db 1691 atgctgtgcctgcactgcccccaaggcgagtcgggagtggcccccaagatgtattcc 1750  
QY 2137 CTGCATATCCAGCTCCGCTTCAAGAGAAAGCTTGCGAGGGCCCAATTTGGGAGGTGACAC 2196  
Db 1751 ctgcattcgcactcgcgttcaagaaagcttgcgagggccagtttgggaggtgaccc 1810  
QY 2197 TGTGTGAGGTGACAGCCCTCAAGATGTGTGATCTTGAATTTCCCTTAATGTGCTA 2256  
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QY 2257 AGGAGACACCTTTTCTGCTGAGCTGTGAAGATCTTACGGCCAGATGACCAAGAATGCCA 2316  
Db 1871 agggacacaccttctgtgtgactgttcaagatcttaacgagcagatgcacacaagatg--- 1927  
QY 2317 GCTTCTCCTGTTCTCGAGGAATGTTCCGTAAGAGAGGTAATGATGCGAGGCTCA 2376  
Db 1928 -----caagaaatgatttccgtgaagaggtgaaaatcaatgctgaggtccta 1972  
QY 2377 AGGACCCCAACATATTCGGCTGCTGGGCGTGTGTGTGACAGAGACCCCTCGCATGA 2436  
Db 1973 aggacccaataatcttcgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2032  
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QY 2497 ACAAGGAGAGCGAGGGGGCCCTGCGGGAACGGGCAAGGCTGGGAGGCCCAACATAGCT 2556  
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QY 3217 GGTGGGCTGGGCCACCCAGAGAGTATGCCCTTCTCCCTTCCCTGAGACACTCTCA 3276  
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QY 3277 TGTCCCTTCTGTTCTTCTCTCTTAAGACCCCTGTGCGCCACCACTGCTGCTGTG 3336  
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QY 3337 ATGGAGTCTCTCCACCCCTCTCTAGCCATCCCTGGGGAGAGGTGGGGAATATATAGC 3396  
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Db 3113 gaatctgggggtgagagagcaagagagagagagaaatgttcttctgtgtgtgtgtgtgt 3172  
QY 3576 ACTTGTCTGAGCTTGGGCTTCTCTCTCTCCCTGATCAGCTGAACACAGTGAACCTGGGGTA 3635  
Db 3173 acttgtctgagccttgggtcttcttcttcttcttcttcttcttcttcttcttcttcttct 3222  
QY 3636 GCCCGCGCCAGCCCTGATCACCCCACTTCCCACTTGGAGTCTTGTAGTGAACATTC 3695  
Db 3233 gccccgcccagccctcagtcacaccccaatcccaactcagctgtgtgtgtgtgtgtgtgt 3292  
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QY 3936 AAAAAAAAAAAAAA 3953  
 Db 3533 acnaaaaaaaaaaaaa 3550

RESULT 6  
 AAC99051 standard; cDNA; 2861 BP.  
 AAC99051;  
 09-MAR-2001 (first entry)

Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:279.

Human: pancreas; pancreatic cancer; pancreatic cancer antigen;  
 detection; diagnosis; identification; cytosolic; neuroprotective;  
 neurotropic; immunomodulatory; relaxant; contractile; gynaecological;  
 antiinflammatory; cardiant; gene therapy; chromosome mapping;  
 linkage analysis; tissue identification; tissue typing; forensic;  
 neural; immune system; muscular; reproductive; gastrointestinal;  
 pulmonary; cardiovascular; renal; proliferative; ss.

OS Homo sapiens.  
 PN MO200055320-A1.  
 PD 21-SEP-2000.  
 PF 08-MAR-2000; 2000MO-US05989.  
 PR 12-MAR-1999; 99US-0124270.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Ruben SM.  
 DR WPI: 2000-579444/54.  
 XX P-PSDB: AAB54286.

PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 treating, or ameliorating a medical condition, particularly pancreatic  
 cancer, or for use in assays for diagnosing a pathological condition -  
 Claim 1: Page 714-715; 1379pp; English.

AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 proteins, called pancreatic cancer antigens, given in AAB54008 to  
 AAB54466. The human pancreatic cancer antigens have cytosolic,  
 neuroprotective, neurotropic, immunomodulatory, relaxant, contractile,  
 gynaecological, cardiant and antiinflammatory activities, and can be used  
 in gene therapy. The polynucleotide and proteins can be used for  
 preventing, treating, or ameliorating a medical condition or in assays  
 for diagnosing a pathological condition or a susceptibility to one in a  
 subject. Binding partners to the proteins and the activity of the  
 proteins can be identified. The pancreatic cancer antigens can be used to  
 detect, treat or prevent pancreatic disorders, especially cancer.  
 Agonists and antagonists to the antigens can be screened for. The  
 pancreatic cancer antigen polynucleotides can be used to design nucleic  
 acid hybridisation probes that can be used in chromosome mapping, linkage  
 analysis, tissue identification and/or typing and a variety of forensic  
 and diagnostic methods. The proteins can be used to generate antibodies  
 which are used to purify, detect and target the polypeptides, including  
 both in vivo and in vitro diagnostic and therapeutic methods. The  
 proteins can be used to treat or prevent neural, immune system, muscular,  
 reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
 sequences used in the exemplification of the present invention.

Sequence 2861 BP; 567 A; 899 C; 800 G; 589 T; 6 other;

Query Match	Best Local Similarity	Score	DB	Length	2861;
Matches	2833; Conservative	5; Mismatches	4; Indels	20; Gaps	3;
QY 1093	GGAGCAACCAAGCTTCTCAGTGTGAGATGAGATTGAGTTGACCGGCTGA	1152			
Db 1	ggacacacacagctctccagtgctatgtgagatgagattgagttgacggtcga	60			
QY 1153	GGGCTTCCAGGCTATGACAGGTCCACTGTAAACAATGACACAGCTGGAGCCGCTTGC	1212			
Db 61	ggccctccagcgtatgacgagttccactgtacaaactgacacgcgtggagccgtctgc	120			
QY 1213	CTGGGGGGGTGGAATGCTTCCCTTCCGGCGTGGCCCTTCCATGCGCTGGAGAGACCCA	1272			
Db 121	ctggcggttgaaatgtcgtctccggtggtcccttcctatggtcgtggagagccca	180			
QY 1273	TGCGCCACAACCTAGGGGSCAACCTGGGGGAGCCCGGAGCCGGGTGCTGAGTGGCCC	1332			
Db 181	tgcgcacaactaggggcaacacctggggaccacagccgggtctctcagtgcccc	240			
QY 1333	TGGGGCGCGTGTGCTGCTTCTGCACTGCGCTTCCCTTTGCGGGGCCCTGTTAC	1392			
Db 241	ttggcgccgtgtgtgtcgtctcttcgtcagtgccgtctctcttcgtgggccccgttac	300			
QY 1393	TCTTCAGGAATCTCTCTCATCTGTGATGTGTGTAACAATCTCTCTCGGACTGGAG	1452			
Db 301	tcttcagcgaactctctctcatctctgtatgtgtgtaacactctctccgacgtggag	360			
QY 1453	GCACCTTCCCGCCAGCCCGCTGTGGGCGCTGGGCGCCACCTCCACAACTTCACAGCT	1512			
Db 361	gcacctcccgccagccccctgtgtggtccggtcccaactcccaacttcagagct	420			
QY 1513	TGGAGCTGGAGCCCAAGAGCCAGACCCGTTGGCCAAAGGCGGAGGCCCGACCGCA	1572			
Db 421	tggagctggagcccgagagccagccgtgtgccaagccgaggggccccgagccgca	480			
QY 1573	TCCCTATGCGGTGCTGGGAGGACATCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1632			
Db 481	tccctatggtcgtccgtgtggtccatcatctctctctctctctctctctctctctct	540			
QY 1633	TCTGGCGGCTGCACTGGGCGAAGGCTCTCAGCAAGGCTGAAAGGAGGCTTGGAGAG	1692			
Db 541	tctggcggtgacgtgacgtgagggaggtgtccacagaaagtggaacggaggtgtgtgaaaggg	600			
QY 1693	AGCTACGCTTCACT	1752			
Db 601	agctacggttcaact	660			
QY 1753	CTAGAGAGCAACCCCGTACAGAGAGGCGCGGCGCTGGGGAATCCGCCACATCCGCTC	1812			
Db 661	ctagagagccaccccccgacagagagcccggtcgtgggaatccgccccacactcgtc	720			
QY 1813	CCTGTGTCCCAATGAGCTCTGCTGTGCTGTCTCTCAATCCAGCTTACCGCTCTCTGG	1872			
Db 721	ccctgtgtcccaatgagctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	780			
QY 1873	CCACTTACGCCGCTCCCTCTGAGGCGCGGCGCCGCCACACCGGCTGGGCCAACCCA	1932			
Db 781	ccacttaagccggtccctctcgtgagcccggtcccccacacgpcgctgtggcaaaccca	840			
QY 1933	CCAAACACCAAGGCTTACAGTGGGAGATATATGAGAGCTGAGAACCGAGCCGCCGCTTC	1992			
Db 841	ccaaacacccaggtccataagtggtgacatataggagcttggaagccagggccccgcttc	900			
QY 1993	TGCCCCACGCTCCCAAGACAGCTCCCAATATGCGAGGCTGAGATGTTATCCCTGTC	2052			
Db 901	tgcgccacactccccaagaaacaggttccccaattatgcggagctgcgaattgttaacctgc	960			
QY 2053	AGGCGTACCGGGGGGAGAACACTATGCTGTGCTGCACTGCCCCCAAGGGGAGTGGGG	2112			
Db 961	aggcggtacacgggggcaaacactatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1020			
QY 2113	ATGGGCCCCCAAGAGTGGATTTCCTCGATCTGACATCGCTTCAAGAGAACGCTTGGCG	2172			







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Db 1543 gctctgttggggaattccaccatcaaatgcagacttggcctagccggaacctc 1602
QY 2713 ATGGGGGACTATTACCGTGGAGGGCGGGGAGTGGTCCGCGCGGAGAGGCT 2772
Db 1603 agcctggggaactataccgtgacgagcgccggcgagtcgcctccacccgcggagggctc 1662
QY 2773 GGGAGTGCATCCTCATGGGGAAGTTACAGACTGCGAGTGAAGTGGGCTTTGGTGA 2832
Db 1663 gggagtgatccctcatctggggaagttcaagactcgagtgagtgaggccttggctgga 1722
QY 2833 CCCTGTGGAGGTGCTGATGCTCTGTAGGGCCAGCCCTTTGGGAGCTCACCGAGAGC 2892
Db 1723 ccttgaggagtgctgtagctctgtagggccagcccttgggagtgaccagcgagc 1782
QY 2893 AGGTATGAGAGAGCGGGGGAGTCTCCGGGACAGGGCGGAGGTGATACCTGTCC 2952
Db 1783 aggtatcgagaaacgggggagtgcttcgcgggaccagggccgggaagtgtaaccgtccc 1842
QY 2953 GGGCCCTGCTGCGCCGAGGGGCTATATAGCTGATGCTTCGGTGTGAGCGGGAGT 3012
Db 1843 ggcgcctgcctgcctcgca-ggcyatatagtctgtagcttccgtgctggagcgggagt 1901
QY 3013 CTGAGCAGCAGACCCCTTTCCAGCTGCATCGGTTCTTGAGAGAGATGCACTCAACA 3072
Db 1902 ctgagcagcagaccaccccttccagctgcacgcgttctcggagagagatcaccaaca 1961
QY 3073 CGGTGTGATACACATCCAGTGGCCCTCCCTGAGGAGATGATCCAGGGGAGGCACTG 3132
Db 1962 cgggtgatacaacataccagctgcctccctccagggagaccaggaagagcagtg 2021
QY 3133 ACATAAAGAGAGAGACATAGGACACTGTGCCCTTCCCTCCGAGAGCCCATCAC 3192
Db 2022 aacataaagagagagacaatagcactctgccttccctcccgacagcccatcacc 2081
QY 3193 TCTATATAGGACAGTGAACACTGCAAGTGGGCTGGGCCACCGAGGAGCTATGCGCTT 3252
Db 2082 tctaataagagcagtgagacgctgagtggtgggtccacacagggagctgagctccctt 2141
QY 3253 CTCCCTTCCTGGACACACTCATGTCCTCCCTTCTCTCTCTCTCTCTCTCTCTCTCT 3312
Db 2142 ctcccttccctggagacacactctcatgtcccttcttcttctctctctctctctct 2201
QY 3313 TCGCCACCCAGCTGGTCTGTGATGGGATCTCTCCACCCCTCTAGCCATCCCTTG 3372
Db 2202 tcgcccacccagctgctctgtagtggaatccctccacccctctctagcatcccttg 2261
QY 3373 GGGAGGAGTGGGAGAAATATAGATAGACACTGACACTGGCCATTTGAGACACTGGCC 3432
Db 2262 gggagaggtggggaatatagatagacactgacactggccatlggacactgggc 2321
QY 3433 CCCACTGGACAACTGATTTCTCTGGAGAGTGGCTGGG-CCCGAGCTCTCTCTCCCTGT 3491
Db 2322 cccactggacaacactgtctctcgagaggtgctgctgcctccacgctctctctccctgt 2381
QY 3492 CACACACTGACCCCACTGCTGAGAAATCTGGGGGTGAGAGGAGCAAGAGAGAGAAA 3551
Db 2382 cacacactgagaccacactgctggaatctgggggtgagaggaagaagagagagaa 2441
QY 3552 ATGTTTCTTGTGCTGTCTCTGTACTGTCTCTGAGCTTGAGGCTTTCTCTCTCTCATCA 3611
Db 2442 atgttctctgtcctgtctctgtactgtctctcagcttggctcttctctccctcatca 2501
QY 3612 CCTGAAACACTGAGACTGGGGGTAGCCCGCCGAGCCCTAGTACACCCCACTTCCAC 3671
Db 2502 cctgaaacactgagactgggggtagcccgccagcccttagtaccaccccaacttccac 2561
QY 3672 TTGAGCTTGTAGCTAGAACTTCTTAAGCCTATAGCTTTCTGTGAGTAATATTGGG 3731
Db 2562 ttgagctctgtagctagaactctctcagcctatagcttctgtgagtaaatattggg 2621
QY 3732 ATTGGGGGAAAGAGGAGCAAGCGCCATAGCTTGGGGTTGACATCTCTAGTGAAC 3791

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Db 2622 attgggggaagagggagcaacggcccatagccttggggttgacatctagtgagc 2681
QY 3792 TGCCACATTAFTTTTCTATATATCACTGGGTTTGTCATTTTGGGGGAGAGACACA 3851
Db 2682 tggccacattgatttctcatalcacttggggttgatcatttgggggagagacaca 2741
QY 3852 GATTTTACACTAATATATATGACACCTAGCTTGAGGCAATTTAATCCCTGCACATGCGAG 3911
Db 2742 gattttcaactaataatataagcctagcttgaggcaatttcaatccctgcactagcag 2801
QY 3912 GTAATATTAAGGTGAGTTTTCACAAAAAAAAAAAAAAA 3953
Db 2802 gtaataataaagtgtagtttccacaaaaaaaaaaaaa 2843

```

## RESULT 8

```

AAV48292
ID AAV48292 standard; cDNA; 3096 BP.
XX
AC AAV48292;
XX
DE 16-NOV-1998 (first entry)
XX
DE Discoidin domain receptor 2 gene.
XX
KW Discoidin domain receptor; transformation; metastasis; collagen; ss;
KW Cleidocranial dysplasia; Stickler syndrome; extracellular matrix; MMP-1.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FH 354..2921
FT CDS
FT /tag= a
FT /product= "Discoidin domain receptor"
FT s1g_peptide 354..416
FT /tag= b
FT mat_peptide 417..2918
FT /tag= c
XX
PN MO9834954-A2.
XX
PD 13-AUG-1998.
XX
PF 05-FEB-1998; 98WO-CA00093.
XX
PR 06-FEB-1997; 97US-0041578.
XX
PA (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX
PI Pawson A, Vogel W;
XX
DR WPI: 1998-447168/38.
XX
DR P-PSDB; AAM77114.
XX
PT Novel ligands of discoidin domain receptor tyrosine kinase,
XX especially collagen - useful for treating e.g. metastasis,
XX cleidocranial dysplasia or Stickler syndrome
XX
PS Disclosure; Fig 22a; 115pp; English.
XX
XX The DDR can be used to identify and evaluate substances which affect DDR
XX receptor tyrosine kinase signalling pathways in the cell. Compounds
XX which modulate such signalling pathways can be used to alter
XX transformation or metastasis in mammals, to treat conditions involving
XX structural or functional deregulation of collagens, e.g. Cleidocranial
XX dysplasia or Stickler syndrome, conditions requiring modulation of
XX extracellular matrix synthesis, degradation or remodelling, or to treat
XX conditions needing modulation of MMP-1 expression such as wound healing.
XX
SQ Sequence 3096 BP; 762 A; 791 C; 752 G; 791 T; 0 other;

```

Query Match

16.2%; Score 642; DB 19; Length 3096;









```

QY 1660 TCAGCAGGCTGAGCGAGGCTGTGTGGAGAGCTGACGGTTACCTCTGTGTCCCTG 1719
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1655 tggagaagctcttcgagagatcgtgatgaaatgcaagtcaccccttcctccaa 1714
QY 1720 GGGAGACTTCCTGCATCAACAACCCGCCAGGTCCTAGAGACCCCGGTACCAAGAC 1779
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1715 gctatctcagatgttccaat-----aaocgtctct 1747
QY 1780 CCCGCCCTGTGGAGATCCGCCCACTCCGCTCCCTGTCCCAATGGCTCTGCTTGC 1839
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1748 catcaccatgtaacaagggtccaaactgactacgactcgtcactt----- 1794
QY 1840 TGTCTCCAAATCCAACCCCTACCCCTCTCTGCGCACTTACGCCGCTCCCTCGAGGCC 1899
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1795 -----ccctctgcgc 1804
QY 1900 GGGGCCCCCACCACCCGCTGTGGCCCAACCCCAACCCAGGCTTACAGTGGGACT 1959
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1805 ctgactaccagagagccatccagctgatacgaanaactccagaattgtctcagaaggag 1864
QY 1960 ATATGAGCCTGAGAGAGCGAGCGCCGCTCTGTGCCCCCACCCTCCGAGAACGGTCC 2019
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1865 agagatcaggtcgcagcggtgtgtgtaagccagtcagccagtgccctgaggagtg 1924
QY 2020 CCCATTATGCGAGGCTGACATTTGTTACCTGACAGGGGCTACCGGGGCAACACTATG 2079
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1925 cccactatgagagctgatacagtaagtaagaccccaagagtgacagaggaacataact 1984
QY 2080 CTGTCCCTGCACTGCCCCAGGGGCAATC-----GGGGATGGGCCCCCAGATGGATTTC 2136
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1985 cagtgccgcgcgcacacacacacacacacacacacacacacacacacacacacacac 2044
QY 2137 CTGATCTGACTCGCTCTTCAAGAGAGCTTGGCGAGGGCCAGTTGGGGAGGGGCAAC 2196
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2045 ccaggaacactcactaacttcaagaagagctgaggaagagacagtttgaggaggtatc 2104
QY 2197 TGTGTGAGGTGACAGCCCTTAAGATCTGTGTCATCTTGTATTTCCCTTAAATGTCGTA 2256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2105 tctgtgaagtgtgaggaatgtgaaatcaagaagaatttgcctcagatgtcagtg 2164
QY 2257 AGGAGACCCCTTGTGTGACTGTGCAAGATCTTACGGCCAGATGCCCAAGATGCCA 2316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2165 ccaaccagcgcctcctcctgagctgtgaaatgtcctcagagagtcacaaagaatg--- 2221
QY 2317 GCTTCTCTTGTCTCCAGAGATATTCTTGAAAGAGGTGAAGTCAATGTCGAGGCA 2376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2222 -----ccaggaatgatttctcctaaggaataaagatctcctgcgcga 2266
QY 2377 AGGACCCCAATATTTGCTGTGCTGTGCTGTGTGTCAGAGACCCCTCTGACATGA 2436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2267 aggaaccaaacatcatcatctatctatctgtgtatcacgtatgacccctctcgtatga 2326
QY 2437 TTAAGTACATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2327 tcaactgataaataagaaatgtgagatcctcaatcagttcttccgcagacagccctca 2386
QY 2497 ACAAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2387 attctctctcagcg-----atgtaagcaactcagtt 2419
QY 2557 ACCCAATGCTGCTGCATGTGGCAGCCAGATGCGCTCCGGCATGCGTATGTGGCAAC 2616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2420 acacacatctgaagtattatgtctacccaattgtcctctgaaatgaatlaacttccctc 2479
QY 2617 TCACCTTGTACATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2676
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2480 ttaatttctgacagagactgtgcacagaaactgtttatgtgtaaaataacacaa 2539
QY 2677 TCAAAATGCGAGATTGGAGATGAGCGGAACTCTATGCTGGGAGTATTATCCGTGTC 2736
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2540 tcaagatagtgacttgatgtgagatgacagaaactgtcagatgtgtgatacttaacagatcc 2599
QY 2737 AGGGCGGAGGAGTGTGCTGCCATCCGCTGTGATGGCTGTGGAAGTGCATCTCATGGGAGAGT 2796

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Db 2600 agggccggcagatgtccctaccctcgtgagtcttctggagagatcttctgctggcaggt 2659
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2797 TCAGCAGCTCGAGTACGAGTGTGGGCTTTGTGTGACCTGTGGGAGGAGTGAAGCT 2856
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2660 tcaactacagaaagtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2719
QY 2857 GTAGGGCCAGCCCTTTGGGCACTCACGAGAGCAGTCAATCAGAGCGGGGAGT 2916
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2720 tcaagaaacagccctattccacagctgtcagatgaaagttatgtgatacttgagagt 2779
QY 2917 TCTTCGGGAGACAGGCGCGGAGGTGTACCTCTCCCGCGCTCTCTCCGACAGGCC 2976
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2780 tctccgaagaccaaaggagagagacttccctcccaaccaaattgtctctgactgt 2839
QY 2977 TATATGAGCTGATGCTGTGCTGTGAGAGCGGAGTGTGAGAGGACACACCTTTCC 3036
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2840 tglataagctgtgtctcagctgtcgtgagaaagataagaaagacccgtcccatcacaag 2899
QY 3037 AGCTGATTCGTTCTT 3052
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2900 aaatccactctgtct 2915

RESULT 11
AAT93784
ID AAT93784 standard; cDNA; 3157 BP.
XX AAT93784;
AC AAT93784;
XX 16-FEB-1998 (first entry)
DT 16-FEB-1998
XX CCK-2, a human mammary carcinoma kinase 10 MCK-10) family member, cDNA.
DE CCK-2, a human mammary carcinoma kinase 10 MCK-10) family member, cDNA.
XX Mammmary carcinoma kinase; MCK-10; CCK-2; receptor tyrosine kinase;
KW proliferative disease; cancer; MCK-10 activity; aberrant expression; ds.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 370..2934
XX FT /*tag= a
XX PN US5677144-A.
XX 14-OCT-1997.
XX 08-NOV-1994; 94US-0336343.
XX 16-NOV-1993; 93US-0153397.
XX (ALVE)/ ALVES F H E.
XX (ULR)/ ULRICH A.
XX PI Alves FHE, Ullrich A;
XX WPI: 1997-511869/47.
XX P-PSDB: AAW34671.
XX Truncated receptor tyrosine kinase CCK-2 - and nucleic acid coding
XX for it, useful for cancer diagnosis
PS Claim 9; Fig 3; 70pp; English.
XX
XX The present sequence represents the cDNA sequence of human CCK-2, a
XX member of the mammary carcinoma kinase 10 (MCK-10, AAT93785) family of
XX receptor tyrosine kinases. Expression of CCK-2 is associated with
XX proliferative diseases such as cancer. The CCK-2 gene was identified by
XX PCR and a cDNA prepared from colonic adenocarcinoma RNA. CCK-2 is
XX expressed in a wide variety of cancer cell lines and tumour tissue. The
XX CCK-2 nucleic acids can be used for diagnostic purposes to detect
XX aberrant expression of CCK-2 genes. Engineered cell lines containing
XX recombinant vectors with the present sequence, are useful for producing

```

CC Infectious retroviral particles. The cell lines may also be used to  
XX evaluate and screen drugs involved in CCK-2 activation and regulation.  
SQ Sequence 3157 BP; 790 A; 802 C; 759 G; 806 T; 0 other;

Query Match 16.2%; Score 642; DB 18; Length 3157;  
Best Local Similarity 56.5%; Pred. No. 1.1e-130;  
Matches 1534; Conservative 0; Mismatches 975; Indels 207; Gaps 10;

QY 349 TGCCTGCTCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 408  
DB 395 TGGTCTGCTCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 454  
QY 409 AGTCCGCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 468  
DB 455 TAGCGCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 514  
QY 469 CCAAGCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 528  
DB 515 CCAAGCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 574  
QY 529 ATGGGCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 585  
DB 575 ATGGGCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 634  
QY 586 TGGATCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 645  
DB 635 TGGATCTGCTGTTGGGACAGTGGAGATGCTGACATGAAGGACATTTGATCTTCCCA 694  
QY 646 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 705  
DB 695 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 754  
QY 706 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 765  
DB 755 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 814  
QY 766 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 825  
DB 815 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 874  
QY 826 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 885  
DB 875 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 934  
QY 886 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 939  
DB 935 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 994  
QY 940 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 999  
DB 995 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1053  
QY 1000 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1059  
DB 1054 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1111  
QY 1060 TGGGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1119  
DB 1112 TGGGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1171  
QY 1120 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1179  
DB 1172 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1231  
QY 1180 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1239  
DB 1232 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1291  
QY 1240 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1299  
DB 1292 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1348

QY 1300 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1359  
DB 1349 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1408  
QY 1360 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1419  
DB 1409 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1468  
QY 1420 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1479  
DB 1469 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1513  
QY 1480 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1539  
DB 1514 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1574  
QY 1540 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1599  
DB 1535 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1654  
QY 1600 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1659  
DB 1595 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1719  
QY 1660 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1719  
DB 1655 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1774  
QY 1720 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1779  
DB 1715 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1839  
QY 1780 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1839  
DB 1748 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1899  
QY 1840 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1899  
DB 1795 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1964  
QY 1900 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1959  
DB 1805 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1984  
QY 1960 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2019  
DB 1865 ATGAGCTGCTGTTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1924  
QY 2020 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2079  
DB 1925 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 1984  
QY 2080 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2136  
DB 1985 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2044  
QY 2137 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2196  
DB 2045 CCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2104  
QY 2197 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2256  
DB 2105 TCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2164  
QY 2257 AGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2316  
DB 2165 AGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2221  
QY 2317 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2376  
DB 2222 GCGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGACAGTGGGAC 2286







```

XX 22-JAN-1999 (first entry)
DT
XX Receptor protein tyrosine kinase (PTK) subtype tyro-10 encoding DNA.
XX
XX PTK: receptor; protein tyrosine kinase; recombinant; grafting;
XX diagnosis; tumour; skin transplant; connective tissue; tyro-10; ss.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 485..3049
XX /tag= a
XX /product= "PTK subtype tyro-10"
XX
XX US5837448-A.
XX
XX 17-NOV-1998.
XX
XX 02-MAY-1994; 94US-0237401.
XX
XX 15-MAY-1992; 92US-0884486.
XX 02-MAY-1994; 94US-0237401.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Lai CHC, Lemke GE;
XX
XX WPI: 1999-023436/02.
XX P-PSDB; AAWB1409.
XX
XX Nucleic acids encoding protein tyrosine kinase subtypes - for
XX identification of new subtypes and treatment of diseases associated
XX with the kinase
XX
XX Claim 1; Columns 53-58; 47pp: English.
XX
XX This DNA encodes a receptor protein tyrosine kinase (PTK) subtype
XX tyro-10. The invention provides sequences AAV65308 to AAV65313, AAV65315,
XX and AAV65317 to AAV65319 that encode proteins having a tyrosine kinase
XX domain and a tissue expression pattern of a receptor PTK subtype selected
XX from tyro-1, tyro-2, tyro-3, tyro-4, tyro-5, tyro-6, tyro-8, tyro-10,
XX tyro-11, and tyro-12, respectively. The polynucleotides are useful for
XX the detection of tyrosine kinase domain sequences and detection of
XX tissue expression patterns of PTK subtypes. The cDNAs can also be
XX injected into oocytes, the protein expressed, and expression products
XX screened for using antibodies against tyrosine kinase epitopes. These
XX subtypes sequences can be used for the design of oligonucleotides, for
XX use in amplification reactions to isolate other subtype sequences. These
XX detection protocols are used in the diagnosis of diseases associated
XX with (receptor) PTKs. Recombinant vectors expressing the subtypes can be
XX used to treat related diseases e.g. tumours, by introduction of the
XX vectors into skin transplants, then grafting these into the connective
XX tissue of the dermis, thus specifically targeting tumours as the
XX proteins are released from the matrix.
XX
XX Sequence 3120 BP; 760 A; 786 C; 830 G; 744 T; 0 other;
XX
XX
XX Query Match 16.1%; Score 639.8; DB 20; Length 3120;
XX Best Local Similarity 56.5%; Prid. No. 3,4e-130;
XX Matches 1552; Conservative 0; Mismatches 987; Indels 210; Gaps 11;
XX
XX 348 CTCTGCTGCTTGGGCGAAGTGGAGTCTGACATGAGAGACATTTTGAATCTGCC 407
XX ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 509 ctggtgctgctctgctcttgcattcctcgtggtctgcaaaagctcaggttaaccagcc 568
XX
XX 408 AAGTGGCGCTATGCCCTGGGAGTACGACGACCATCCAGACAGTGAATCTGCT 467
XX ||| ||||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
XX 569 atatgctgctatctcttggtcagtgagagacattccagatgagacattcaagcc 628
XX
XX 468 TCCAGTCTCTGTGTCATATTCATGCGCCCGCCACAGCAGGTGGAGAGACAGTACGGG 527
XX ||| ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 629 tcaagtcagtggtcagaatccacagctgcacaatatggaagctgagcctctgaagaaga 688
QY 528 GATGGGCGCTGTGTCGCCCGCAGGGGTGCTTTCCCAAGGA---GGAGAGTACTTGCAG 584
XX ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 689 gatgagcctgtgtcctcttgatattccagtgcaaccagctgactggaagattctgcag 748
QY 585 GTGAGTCTCAACAGATCTCACCTGTGCTGTGTGGACCCAGGAGCGCATGCGCGG 644
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 749 atgacttggaaccctacattatcactctgtgtggaagccaggggycgcatgaagg 808
QY 645 GGCCTGGCAAGAGATTCTCCGAGACTACCGGCTGCTTACCTCCGGATGTTGGCGGC 704
XX ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 809 ggtcagtgatggaattgacacccatgatacaatacagtcggaatggcagtcgc 868
QY 705 TGGATGGCTGGAAGAGACCGCTGGGTCAGAGGTGATCTCAGGCAATGAGACCCCTGAG 764
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QY 885 GATGACATCTGCTTACACCGCCCGCTGGGCGCAGACATGATTATCTGAGG----- 939
XX ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 940 -CCGTACTCTAAGAGACTCCACCTATGACGACATACCCTGGGCGCATGCAATGAGG 998
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XX ||| ||||| ||| ||| ||| ||| ||| ||||| ||| ||| ||| |||
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XX ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1239 CGTGGCCCTGCAATGAGCTGTGAGAGGAGGAGCCCATGCGCCCAACATGAGGCGCA 1298
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QY 1359 CAGTGGCGCTTCTCTTGTGCGGGCGGCTTACTCTTCAAGCAAAATCTTATCTG 1418
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XX ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 1539 CCGTGGCCAAAGCGAGGAGGAGCCGACGCTTCACTGAGGCTGCTGTGAGGCGATG 1598
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Oy 1049 GAGTCAGGAGCTCGGGTCTGG 1070  
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Job time: 19933 sec